

Product datasheet for **SC329698**

ATP6V1G2 (NM_001204078) Human Untagged Clone

Product data:

Product Type: Expression Plasmids
Product Name: ATP6V1G2 (NM_001204078) Human Untagged Clone
Tag: Tag Free
Symbol: ATP6V1G2
Synonyms: ATP6G; ATP6G2; NG38; VMA10
Vector: pCMV6-Entry (PS100001)
Fully Sequenced ORF: >SC329698 representing NM_001204078.
Blue=Insert sequence Red=Cloning site Green=Tag(s)

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ATGGCCAGTCAGTCCCAAGGTATCCAGCAGCTTCTGCAAGCTGAGAAGCGGGCAGCTGAGAAGGTGGCA
GATGCCAGAAAGAGGAAGGCCCGCGACTGAAGCAGGCTACAAGGCGCCAGGTGCAGGGCATGCAGAGC
TCCAGCAGAGAAACCGAGAGCGTGTCTGGCCAGCTTCTTGGCATGGTCTGCGACGTCAGGCCCCAG
GTCCACCCCAACTACCGATTCTGCTAG
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Restriction Sites: SgfI-MluI
ACCN: NM_001204078
Insert Size: 237 bp

OTI Disclaimer: Our molecular clone sequence data has been matched to the reference identifier above as a point of reference. Note that the complete sequence of our molecular clones may differ from the sequence published for this corresponding reference, e.g., by representing an alternative RNA splicing form or single nucleotide polymorphism (SNP).

Components: The ORF clone is ion-exchange column purified and shipped in a 2D barcoded Matrix tube containing 10ug of transfection-ready, dried plasmid DNA (reconstitute with 100 ul of water).

Reconstitution Method:

1. Centrifuge at 5,000xg for 5min.
2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA.
3. Close the tube and incubate for 10 minutes at room temperature.
4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom.
5. Store the suspended plasmid at -20°C. The DNA is stable for at least one year from date of shipping when stored at -20°C.

RefSeq: [NM_001204078.1](#)



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RefSeq Size:	1483 bp
RefSeq ORF:	237 bp
Locus ID:	534
UniProt ID:	O95670
Cytogenetics:	6p21.33
Protein Pathways:	Epithelial cell signaling in Helicobacter pylori infection, Metabolic pathways, Oxidative phosphorylation, Vibrio cholerae infection
MW:	9 kDa
Gene Summary:	<p>This gene encodes a component of vacuolar ATPase (V-ATPase), a multisubunit enzyme that mediates acidification of intracellular compartments of eukaryotic cells. V-ATPase dependent acidification is necessary for such intracellular processes as protein sorting, zymogen activation, receptor-mediated endocytosis, and synaptic vesicle proton gradient generation. V-ATPase is composed of a cytosolic V1 domain and a transmembrane V0 domain. The V1 domain consists of three A and three B subunits, two G subunits plus the C, D, E, F, and H subunits. The V1 domain contains the ATP catalytic site. The V0 domain consists of five different subunits: a, c, c', c'', and d. Additional isoforms of many of the V1 and V0 subunit proteins are encoded by multiple genes or alternatively spliced transcript variants. This encoded protein is one of three V1 domain G subunit proteins. This gene had previous gene symbols of ATP6G and ATP6G2. Alternatively spliced transcript variants encoding different isoforms have been described. Read-through transcription also exists between this gene and the downstream DEAD (Asp-Glu-Ala-Asp) box polypeptide 39B (DDX39B) gene. [provided by RefSeq, Feb 2011]</p> <p>Transcript Variant: This variant (3) uses two alternate splice sites that result in the loss of an in-frame segment in the central coding region, compared to variant 1. The encoded isoform (c) is shorter than isoform a.</p>